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<110> Benkovic, Stephen J
 <120> Treatment of Bacterial Induced Diseases Using DNA Methyl
 Transferase Inhibitors
 <130> 00-387-P
 <140> To be Assigned
 <141> Herewith
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 <151> 2001-11-29
 <150> US 09/578,991
 <151> 2000-05-25
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 gcggcgcttg gacgatgact cctgcggcga cgaaaatccc tcgggcgctc tcaggctttg 240
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cca atg tca tca gtt gtt tcg ctt gcc gaa atc tcc cgt gcc gcc cgt	348
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Pro Leu Asn Trp Leu Asp Ser Ile Ile Lys Gly Asp Cys Val Ala Ala	
20 25 30	
ctg aac gcg ctt ccc gat cat tcg gtc gat gtc gtc ttc gcc gac ccg	444
Leu Asn Ala Leu Pro Asp His Ser Val Asp Val Val Phe Ala Asp Pro	
35 40 45	
ccc tat aat ctt cag ctc ggc ggc acg ttg cac cgg ccc gat cag tcg	492
Pro Tyr Asn Leu Gln Leu Gly Gly Thr Leu His Arg Pro Asp Gln Ser	
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ctg gtc gat gca gtg gac gac gat tgg gac cag ttt gct tcc ttc gaa	540
Leu Val Asp Ala Val Asp Asp Asp Trp Asp Gln Phe Ala Ser Phe Glu	
65 70 75	
gcc tat gac gct ttc acc cgc gcc tgg ctg ctt gcc tgc cgg cgt gtc	588
Ala Tyr Asp Ala Phe Thr Arg Ala Trp Leu Leu Ala Cys Arg Arg Val	
80 85 90 95	
ctg aag ccc acc ggc acg ctc tgg gtc atc ggt tcc tac cac aat atc	636
Leu Lys Pro Thr Gly Thr Leu Trp Val Ile Gly Ser Tyr His Asn Ile	
100 105 110	
ttc cgg gtc ggc gcg atc ctc cag gac ctg cac ttc tgg gtc ttg aac	684
Phe Arg Val Gly Ala Ile Leu Gln Asp Leu His Phe Trp Val Leu Asn	
115 120 125	
gat atc atc tgg cgc aag acc caa ccc gat gcc gaa ctt caa ggg cgc	732
Asp Ile Ile Trp Arg Lys Thr Gln Pro Asp Ala Glu Leu Gln Gly Arg	
130 135 140	
cgc ttc cag aac gcg cat gaa acg ctg atc tgg gcg acg gcg aac gcc	780
Arg Phe Gln Asn Ala His Glu Thr Leu Ile Trp Ala Thr Ala Asn Ala	
145 150 155	
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Lys Ala Lys Gly Tyr Thr Phe Asn Tyr Glu Ala Met Lys Ala Ala Asn	
160 165 170 175	
gac gac gtt cag atg cgc tcc gac tgg ctg ttc ccc atc tgc tcc ggt	876
Asp Asp Val Gln Met Arg Ser Asp Trp Leu Phe Pro Ile Cys Ser Gly	
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tcc gag cgg ctg aag ggc gac gac ggc aag aaa gta cac ccg acg caa	924
Ser Glu Arg Leu Lys Gly Asp Asp Gly Lys Lys Val His Pro Thr Gln	
195 200 205	
aag ccg gaa gcg ctg ctt gcc cgc atc ctg atg gcc tcg acc aag ccc	972
Lys Pro Glu Ala Leu Leu Ala Arg Ile Leu Met Ala Ser Thr Lys Pro	
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gtc gcc aag cgc ctc ggc cgg cac ttc gtc ggg atc gag cgc gag cag Val Ala Lys Arg Leu Gly Arg His Phe Val Gly Ile Glu Arg Glu Gln 240 245 250 255	1068
gac tat atc gat gcc gcc gcc gaa cgt atc gcg gcc gtg gag ccg ctc Asp Tyr Ile Asp Ala Ala Ala Glu Arg Ile Ala Ala Val Glu Pro Leu 260 265 270	1116
ggc aag gcc acg ctc tcg gtc atg acc ggc aag aag gcg gag ccg cgc Gly Lys Ala Thr Leu Ser Val Met Thr Gly Lys Lys Ala Glu Pro Arg 275 280 285	1164
gtc gcc ttc aac act ctg gtg gaa agc ggg ctc atc aag ccc ggc acg Val Ala Phe Asn Thr Leu Val Glu Ser Gly Leu Ile Lys Pro Gly Thr 290 295 300	1212
gtt ctg acg gat gcg aag cgc cgc tac agc gcg atc gtc cgc gcc gac Val Leu Thr Asp Ala Lys Arg Arg Tyr Ser Ala Ile Val Arg Ala Asp 305 310 315	1260
ggc acg ctg gcg tcc ggc ggc gag gct gga tcc att cac cgc ctc ggc Gly Thr Leu Ala Ser Gly Gly Glu Ala Gly Ser Ile His Arg Leu Gly 320 325 330 335	1308
gca aaa gtg cag ggc ctc gac gcc tgc aac ggc tgg acc ttc tgg cac Ala Lys Val Gln Gly Leu Asp Ala Cys Asn Gly Trp Thr Phe Trp His 340 345 350	1356
ttc gag gag gga agc gta ttg aaa ccg atc gac gag ctc aga tcc gtc Phe Glu Glu Gly Ser Val Leu Lys Pro Ile Asp Glu Leu Arg Ser Val 355 360 365	1404
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 35 40 45
 Tyr Asn Leu Gln Leu Gly Gly Thr Leu His Arg Pro Asp Gln Ser Leu
 50 55 60
 Val Asp Ala Val Asp Asp Asp Trp Asp Gln Phe Ala Ser Phe Glu Ala
 65 70 75 80
 Tyr Asp Ala Phe Thr Arg Ala Trp Leu Leu Ala Cys Arg Arg Val Leu
 85 90 95
 Lys Pro Thr Gly Thr Leu Trp Val Ile Gly Ser Tyr His Asn Ile Phe
 100 105 110
 Arg Val Gly Ala Ile Leu Gln Asp Leu His Phe Trp Val Leu Asn Asp
 115 120 125
 Ile Ile Trp Arg Lys Thr Gln Pro Asp Ala Glu Leu Gln Gly Arg Arg
 130 135 140
 Phe Gln Asn Ala His Glu Thr Leu Ile Trp Ala Thr Ala Asn Ala Lys
 145 150 155 160
 Ala Lys Gly Tyr Thr Phe Asn Tyr Glu Ala Met Lys Ala Ala Asn Asp
 165 170 175
 Asp Val Gln Met Arg Ser Asp Trp Leu Phe Pro Ile Cys Ser Gly Ser
 180 185 190
 Glu Arg Leu Lys Gly Asp Asp Gly Lys Lys Val His Pro Thr Gln Lys
 195 200 205
 Pro Glu Ala Leu Leu Ala Arg Ile Leu Met Ala Ser Thr Lys Pro Gly
 210 215 220

Asp Val Val Leu Asp Pro Phe Phe Gly Ser Gly Thr Thr Gly Ala Val
225 230 235 240

Ala Lys Arg Leu Gly Arg His Phe Val Gly Ile Glu Arg Glu Gln Asp
245 250 255

Tyr Ile Asp Ala Ala Ala Glu Arg Ile Ala Ala Val Glu Pro Leu Gly
260 265 270

Lys Ala Thr Leu Ser Val Met Thr Gly Lys Lys Ala Glu Pro Arg Val
275 280 285

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290 295 300

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Thr Leu Ala Ser Gly Gly Glu Ala Gly Ser Ile His Arg Leu Gly Ala
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Arg Asn Asp Leu Ala Lys Leu Asn
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gccgttccag ccttgacacat ggatcacgtc gtcacgatga caactcgata attatctctg	240
ccttattggg cgcgcaaagg ccgcaaagcc gggctttccc tgtgatatta agaaaagatt	300
taggatttca agcacttggc gttaagcgca tattttaccct aggcagtaac cataggaaca	360
agttttttgc gttcacaggt aatcgagtat ccc atg tcc cta gta cgt ctt gcg	414
Met Ser Leu Val Arg Leu Ala	
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cat gag ttg ccc atc gag gcc ccg cgt acc gcc tgg ctc gac tcc atc	462
His Glu Leu Pro Ile Glu Ala Pro Arg Thr Ala Trp Leu Asp Ser Ile	
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atc aaa ggt gat tgc gtt tcc gcg ctg gag cgc ctg ccg gat cat tcc	510
Ile Lys Gly Asp Cys Val Ser Ala Leu Glu Arg Leu Pro Asp His Ser	
25 30 35	
gta gac gtc atc ttt gcc gat ccg ccc tat aat ctc cag ctt ggc ggc	558
Val Asp Val Ile Phe Ala Asp Pro Pro Tyr Asn Leu Gln Leu Gly Gly	
40 45 50 55	
gat ctg cac cgt ccg gat cag tcc atg gtc agc gcc gtg gac gat cat	606
Asp Leu His Arg Pro Asp Gln Ser Met Val Ser Ala Val Asp Asp His	
60 65 70	
tgg gac cag ttt gaa agc ttc cag gcc tat gac gcc ttc acc cgc gcc	654
Trp Asp Gln Phe Glu Ser Phe Gln Ala Tyr Asp Ala Phe Thr Arg Ala	
75 80 85	
tgg ctg ctc gcc tgc cgc cgt gtg ctg aag ccg aat ggc acc atc tgg	702
Trp Leu Leu Ala Cys Arg Arg Val Leu Lys Pro Asn Gly Thr Ile Trp	
90 95 100	
gtc atc ggt tcc tat cac aat att ttc cgc gtc ggc acg cag ttg cag	750
Val Ile Gly Ser Tyr His Asn Ile Phe Arg Val Gly Thr Gln Leu Gln	
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gat ctg ggc ttc tgg ctc ctc aac gac att gtc tgg cgc aag acc aat	798
Asp Leu Gly Phe Trp Leu Leu Asn Asp Ile Val Trp Arg Lys Thr Asn	
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Pro Met Pro Asn Phe Arg Gly Arg Arg Phe Gln Asn Ala His Glu Thr	
140 145 150	
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Leu Ile Trp Ala Ser Arg Glu Gln Lys Gly Lys Gly Tyr Thr Phe Asn	
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tac gag ggc atg aaa gcg gcc aat gac gat gtg cag atg cgt tcg gac	942
Tyr Glu Gly Met Lys Ala Ala Asn Asp Asp Val Gln Met Arg Ser Asp	
170 175 180	
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Trp Leu Phe Pro Ile Cys Thr Gly Ser Glu Arg Leu Lys Asp Glu Asn	
185 190 195	

ggc gac aag gtc cac ccg acc cag aag ccg gaa gca ctt ctc gcg cgc	1038
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Phe Val Gly Ile Glu Arg Glu Gln Pro Tyr Ile Asp Ala Ala Thr Ala	
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Arg Ile Asn Ala Val Glu Pro Leu Gly Lys Ala Glu Leu Thr Val Met	
265 270 275	
acc ggc aag cgc gca gag ccg cgc gtg gcc ttc acg agc gta atg gaa	1278
Thr Gly Lys Arg Ala Glu Pro Arg Val Ala Phe Thr Ser Val Met Glu	
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Ala Gly Leu Leu Arg Pro Gly Thr Val Leu Cys Asp Glu Arg Arg Arg	
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Phe Ala Ala Ile Val Arg Ala Asp Gly Thr Leu Thr Ala Asn Gly Glu	
315 320 325	
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Ala Gly Ser Ile His Arg Ile Gly Ala Arg Val Gln Gly Phe Asp Ala	
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Cys Asn Gly Trp Thr Phe Trp His Phe Glu Glu Asn Gly Val Leu Lys	
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Pro Ile Asp Ala Leu Arg Lys Ile Ile Arg Glu Gln Met Ala Ala Ala	
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Gly Ala	
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Tyr Asn Leu Gln Leu Gly Gly Asp Leu His Arg Pro Asp Gln Ser Met
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Val Ser Ala Val Asp Asp His Trp Asp Gln Phe Glu Ser Phe Gln Ala
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Tyr Asp Ala Phe Thr Arg Ala Trp Leu Leu Ala Cys Arg Arg Val Leu
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Lys Pro Asn Gly Thr Ile Trp Val Ile Gly Ser Tyr His Asn Ile Phe
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Arg Val Gly Thr Gln Leu Gln Asp Leu Gly Phe Trp Leu Leu Asn Asp
 115 120 125

Ile Val Trp Arg Lys Thr Asn Pro Met Pro Asn Phe Arg Gly Arg Arg
 130 135 140

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 145 150 155 160

Gly Lys Gly Tyr Thr Phe Asn Tyr Glu Gly Met Lys Ala Ala Asn Asp
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Asp Val Gln Met Arg Ser Asp Trp Leu Phe Pro Ile Cys Thr Gly Ser
 180 185 190

Glu Arg Leu Lys Asp Glu Asn Gly Asp Lys Val His Pro Thr Gln Lys
 195 200 205

Pro Glu Ala Leu Leu Ala Arg Ile Met Met Ala Ser Ser Lys Pro Gly
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Asp Val Ile Leu Asp Pro Phe Phe Gly Ser Gly Thr Thr Gly Ala Val
 225 230 235 240

Ala Lys Arg Leu Gly Arg His Phe Val Gly Ile Glu Arg Glu Gln Pro
 245 250 255

Tyr Ile Asp Ala Ala Thr Ala Arg Ile Asn Ala Val Glu Pro Leu Gly
 260 265 270

Lys Ala Glu Leu Thr Val Met Thr Gly Lys Arg Ala Glu Pro Arg Val
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Ala Phe Thr Ser Val Met Glu Ala Gly Leu Leu Arg Pro Gly Thr Val
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Leu Cys Asp Glu Arg Arg Arg Phe Ala Ala Ile Val Arg Ala Asp Gly
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Thr Leu Thr Ala Asn Gly Glu Ala Gly Ser Ile His Arg Ile Gly Ala
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Arg	Pro	Asp	Gln	Ser	Leu	Val	Asp	Ala	Val	Asp	Asp	Glu	Trp	Asp	Gln		
			20					25					30				
ttc	gcc	tcc	ttc	gac	gcc	tat	gac	gcc	ttc	acc	cgc	gcc	tgg	ctg	ctc		144
Phe	Ala	Ser	Phe	Asp	Ala	Tyr	Asp	Ala	Phe	Thr	Arg	Ala	Trp	Leu	Leu		
		35					40					45					
gcc	tgc	cgc	cgt	gtg	ctg	aaa	ccg	aac	ggc	acc	atc	tgg	gtc	atc	ggc		192
Ala	Cys	Arg	Arg	Val	Leu	Lys	Pro	Asn	Gly	Thr	Ile	Trp	Val	Ile	Gly		
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tcc	tat	cac	aat	atc	ttc	cgc	gtc	ggc	gcc	atg	ctc	cag	aac	ctc	gat		240
Ser	Tyr	His	Asn	Ile	Phe	Arg	Val	Gly	Ala	Met	Leu	Gln	Asn	Leu	Asp		
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Phe	Trp	Ile	Leu	Asn													
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Phe	Ala	Ser	Phe	Asp	Ala	Tyr	Asp	Ala	Phe	Thr	Arg	Ala	Trp	Leu	Leu		
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Ala	Cys	Arg	Arg	Val	Leu	Lys	Pro	Asn	Gly	Thr	Ile	Trp	Val	Ile	Gly		
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Ser	Tyr	His	Asn	Ile	Phe	Arg	Val	Gly	Ala	Met	Leu	Gln	Asn	Leu	Asp		
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gctagggact aaacattaag atagccttaa aacgcttggtg ttaaaatggc cagagtagca      180
gatataaaag gctagttaat c atg gat ttt tta aaa gaa aac tta aac act      231
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Ile Ile Glu Gly Asp Cys Leu Glu Lys Leu Lys Asp Phe Pro Asn Lys
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Ser Val Asp Phe Ile Phe Ala Asp Pro Pro Tyr Phe Met Gln Thr Glu
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Gly Glu Leu Lys Arg Phe Glu Gly Thr Lys Phe Gln Gly Val Glu Asp
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cat tgg gat aaa ttt ggc tct ttt gaa gaa tac gat acc ttt tgt ttg      423
His Trp Asp Lys Phe Gly Ser Phe Glu Glu Tyr Asp Thr Phe Cys Leu
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ggg tgg tta aaa gaa tgc caa agg att tta aaa gat aat ggc act att      471
Gly Trp Leu Lys Glu Cys Gln Arg Ile Leu Lys Asp Asn Gly Thr Ile
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tgt gtg ata ggg act ttt caa aat att ttt aga att ggt ttt cat ttg      519
Cys Val Ile Gly Thr Phe Gln Asn Ile Phe Arg Ile Gly Phe His Leu
                        95          100          105
caa aat tta ggg ttt tgg ata ctc aat gat att gtt tgg tac aag agc      567
Gln Asn Leu Gly Phe Trp Ile Leu Asn Asp Ile Val Trp Tyr Lys Ser
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Asn Pro Val Pro Asn Phe Ala Gly Lys Arg Leu Cys Asn Ala His Glu
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acg ctt att tgg tgc gct aaa cac aaa aac aac aaa gtt acc ttt aat      663
Thr Leu Ile Trp Cys Ala Lys His Lys Asn Asn Lys Val Thr Phe Asn
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Tyr Lys Thr Met Lys Tyr Leu Asn Asn Asn Lys Gln Glu Lys Ser Val
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Gly Lys Lys Val His Ser Thr Gln Lys Pro Glu Ala Leu Leu Lys Lys	190	195	200	
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Phe Gly Thr Gly Thr Thr Gly Ala Val Ala Lys Ser Met Asn Arg Tyr	220	225	230	
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Phe Ile Gly Ile Glu Lys Asp Ser Phe Tyr Ile Lys Glu Ala Ala Lys	235	240	245	250
cgc ctt aat agc act agg gat aaa agc gat ttt atc act aat tta gat				999
Arg Leu Asn Ser Thr Arg Asp Lys Ser Asp Phe Ile Thr Asn Leu Asp	255	260	265	
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Leu Glu Thr Lys Pro Pro Lys Ile Pro Met Ser Leu Leu Ile Ser Lys	270	275	280	
caa tta ctc aaa att gga gat ttt tta tac tca tct aac aaa gaa aaa				1095
Gln Leu Leu Lys Ile Gly Asp Phe Leu Tyr Ser Ser Asn Lys Glu Lys	285	290	295	
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gaa act tct att cat aag atg agc gct aaa tat ttg aat aaa act aac				1191
Glu Thr Ser Ile His Lys Met Ser Ala Lys Tyr Leu Asn Lys Thr Asn	315	320	325	330
cat aat ggc tgg aaa ttt ttt tat gcg tat tac caa aat caa ttt tta				1239
His Asn Gly Trp Lys Phe Phe Tyr Ala Tyr Tyr Gln Asn Gln Phe Leu	335	340	345	
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Leu Leu Asp Glu Leu Arg Tyr Ile Cys Gln Arg Asp Ser	350	355		
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 agtgcgatgg cgtgaaacct tagccgattt agccagtttg aattttgatg aaaatccttt 1948
 agaaagtttt agagaaatca aagatttagc gccaagcgtt tataggaagc ttttgataa 2008
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<400> 8

Met Asp Phe Leu Lys Glu Asn Leu Asn Thr Ile Ile Glu Gly Asp Cys
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Leu Glu Lys Leu Lys Asp Phe Pro Asn Lys Ser Val Asp Phe Ile Phe
 20 25 30

Ala Asp Pro Pro Tyr Phe Met Gln Thr Glu Gly Glu Leu Lys Arg Phe
 35 40 45

Glu Gly Thr Lys Phe Gln Gly Val Glu Asp His Trp Asp Lys Phe Gly
 50 55 60

Ser Phe Glu Glu Tyr Asp Thr Phe Cys Leu Gly Trp Leu Lys Glu Cys
 65 70 75 80

Gln Arg Ile Leu Lys Asp Asn Gly Thr Ile Cys Val Ile Gly Thr Phe
 85 90 95

Gln Asn Ile Phe Arg Ile Gly Phe His Leu Gln Asn Leu Gly Phe Trp
 100 105 110

Ile Leu Asn Asp Ile Val Trp Tyr Lys Ser Asn Pro Val Pro Asn Phe
115 120 125

Ala Gly Lys Arg Leu Cys Asn Ala His Glu Thr Leu Ile Trp Cys Ala
130 135 140

Lys His Lys Asn Asn Lys Val Thr Phe Asn Tyr Lys Thr Met Lys Tyr
145 150 155 160

Leu Asn Asn Asn Lys Gln Glu Lys Ser Val Trp Gln Ile Pro Ile Cys
165 170 175

Met Gly Asn Glu Arg Leu Lys Asp Ala Gln Gly Lys Lys Val His Ser
180 185 190

Thr Gln Lys Pro Glu Ala Leu Leu Lys Lys Ile Ile Leu Ser Ala Thr
195 200 205

Lys Pro Lys Asp Ile Ile Leu Asp Pro Phe Phe Gly Thr Gly Thr Thr
210 215 220

Gly Ala Val Ala Lys Ser Met Asn Arg Tyr Phe Ile Gly Ile Glu Lys
225 230 235 240

Asp Ser Phe Tyr Ile Lys Glu Ala Ala Lys Arg Leu Asn Ser Thr Arg
245 250 255

Asp Lys Ser Asp Phe Ile Thr Asn Leu Asp Leu Glu Thr Lys Pro Pro
260 265 270

Lys Ile Pro Met Ser Leu Leu Ile Ser Lys Gln Leu Leu Lys Ile Gly
275 280 285

Asp Phe Leu Tyr Ser Ser Asn Lys Glu Lys Ile Cys Gln Val Leu Glu
290 295 300

Asn Gly Gln Val Arg Asp Asn Glu Asn Tyr Glu Thr Ser Ile His Lys
305 310 315 320

Met Ser Ala Lys Tyr Leu Asn Lys Thr Asn His Asn Gly Trp Lys Phe
325 330 335

Phe Tyr Ala Tyr Tyr Gln Asn Gln Phe Leu Leu Leu Asp Glu Leu Arg

340

345

350

Tyr Ile Cys Gln Arg Asp Ser
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<210> 9
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<220>
<223> Description of Artificial Sequence: Forward primer (IFADPPY)

<400> 9
atyttygcbg ayccbcbta 20

<210> 10
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<220>
<223> Description of Artificial Sequence: Reverse primer 1 (LDPFFG)

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ccraaraavg grtcsag 17

<210> 11
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Reverse primer 2 (IGIERE)

<400> 11
tcvcgytcra tvccrat 17

<210> 12
<211> 17
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<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 12
actcgcgagt caacaga 17

<210> 13
<211> 23

<212> DNA
 <213> Artificial

 <220>
 <223> Description of Artificial Sequence: oligonucleotide

 <400> 13
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 <210> 14
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 <223> Description of Artificial Sequence: oligonucleotide

 <400> 14
 tcctctcgcg agtcaacaga aat 23

 <210> 15
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<220>
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<400> 18
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<210> 19
 <211> 51
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<220>
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<400> 19
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<400> 20
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<210> 21
 <211> 51

<212> DNA
 <213> Artificial

 <220>
 <223> Description of Artificial Sequence: oligonucleotide

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 <210> 22
 <211> 60
 <212> DNA
 <213> Artificial

 <220>
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 <400> 22
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 agagga 66

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